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<110> Monsanto Company

<120> TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROL
COMPOUNDS AND TOCOPHEROLS

<130> MTC 6462.1

<140> 09/548,256

<141> 2000-04-12

<150> 60/128,995

<151> 1999-04-12

<160> 31

<170> PatentIn Ver. 2.1

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<212> PRT

<213> jojoba

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Val Val Phe Lys Asp Leu Gly Ala Gln Val Ser Tyr Arg Thr Leu Phe
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Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr
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Phe Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Cys Val Ile His
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Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
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Arg Ile Leu Glu Thr Phe Phe Val His Arg Phe Ser His Thr Ser Pro
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Ile Gly Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Ser Phe Gly Ala
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Tyr Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser Asp
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Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val Ala
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Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Ser Gly
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Ala Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr
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Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn Ile
 245 250 255

Ala Thr Gln Thr Ile Ala Gly Tyr Val Phe Leu Ala Val Ala Ala Leu
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Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys Ile
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Leu Pro Pro Phe Leu
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      20              25              30

Ile His Ala Arg Thr Lys Lys Tyr Tyr Pro Ser Arg Gln Arg Leu Thr
      35              40              45

Leu Pro Leu Gln Pro Gly Lys Gly Gly Lys Pro Val Val Leu Ser Pro
      50              55              60

Lys Ala Ser Leu Leu Glu Tyr Cys Glu Lys Gly Ser Gly Ser Leu Thr
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Val Val Phe Lys Asp Leu Gly Pro Gln Val Tyr Tyr Ser Thr Leu Phe
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Phe Phe Glu Tyr Leu Gly Pro Leu Ile Ile Tyr Pro Met Phe Tyr Tyr
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Leu Pro Val Tyr Lys Tyr Phe Gly His Glu Gly Glu Arg Ala Met His
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Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
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Arg Ile Met Glu Thr Phe Phe Val His Arg Phe Ser Ala Thr Ser Pro
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Leu Ser Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Thr Phe Gly Ala
 165 170 175

Tyr Ile Ala Tyr Tyr Cys Asn His Pro Leu Tyr Thr Pro Val Ser Asp
 180 185 190

Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Val Val Cys Gln Val Ala
 195 200 205

Asn Phe Tyr Cys His Ile Leu Leu Arg Asn Leu Arg Ser Pro Ser Gly
 210 215 220

Ser Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr
 225 230 235 240

Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Val Gly Phe Asn Ile
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Ala Thr Gln Thr Val Ala Gly Tyr Val Phe Leu Val Val Ala Ala Gly
 260 265 270

Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Lys Lys Leu
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Phe Asp Gly Lys Asp Gly Arg Pro Lys Tyr Pro Arg Arg Trp Val Ile
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Leu Pro Pro Phe Leu
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 35 40 45

Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu Ala Ser Phe Trp Ile Phe
 50 55 60

Pro His Gln Gly Leu Arg Ser Thr Leu Leu Gln Ser Ala Val Thr Leu
 65 70 75 80

His Phe Phe Lys Arg Val Phe Glu Val Val Phe Ile His Lys Tyr Ser
 85 90 95

Gly Ala Met Leu Leu Asp Ser Ala Ile Pro Ile Thr Leu Ser Tyr Phe
 100 105 110

Leu Ser Thr Ala Thr Met Ile Tyr Ala Gln His Leu Thr Gln Gly Leu
 115 120 125

Pro Glu Pro Pro Ile Asp Leu Leu Tyr Pro Gly Ile Val Leu Phe Val
 130 135 140

Val Gly Ile Ile Gly Asn Phe Tyr His His Tyr Leu Leu Ser Asn Leu
 145 150 155 160

Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile Pro Lys Gly Gly Met Phe
165 170 175

Glu Leu Val Ile Cys Pro His Tyr Leu Phe Glu Ile Ile Glu Phe Tyr
180 185 190

Gly Phe Ser Phe Ile Ser Gln Thr Leu Tyr Ala Phe Ser Phe Thr Val
195 200 205

Gly Thr Thr Leu Tyr Leu Leu Gly Arg Ser Tyr Ser Thr Arg Lys Trp
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Tyr Leu Ser Lys Phe Glu Asp Phe Pro Glu His Val Lys Ala Ile Ile
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Asn Ala Phe Leu Ser Glu Ile Arg Gly Lys His Leu Asn Tyr Ser Lys
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Phe Trp Asn Ala Asn Pro Ser Ala Glu Lys Gln Val Lys Leu Ser Ser
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Lys Ala Gly Met Leu Leu Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu
65 70 75 80

Ala Ser Phe Trp Val Phe Pro His Gln Gly Leu Arg Phe Thr Ile Leu
85 90 95

Gln Ser Ala Val Thr Leu His Tyr Phe Lys Arg Val Phe Glu Gly Leu
100 105 110

Phe Ile His Lys Tyr Ser Gly Gly Met Thr Leu Glu Ser Ala Ile Pro
115 120 125

Ile Thr Leu Ser Tyr Phe Leu Ser Ala Val Thr Met Val Tyr Ser Gln
130 135 140

His Leu Thr Lys Gly Phe Pro Glu Pro Pro Ile Asn Leu Phe Tyr Pro
145 150 155 160

Gly Ile Val Leu Phe Leu Val Gly Ile Ile Gly Asn Phe Tyr His His
165 170 175

Tyr Leu Leu Ser Lys Leu Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile
180 185 190

Pro Lys Gly Gly Phe Phe Glu Leu Val Ile Cys Pro His Tyr Phe Phe
195 200 205

Glu Ile Thr Val Phe Tyr Gly Ile Phe Phe Ile Ser Gln Thr Leu Tyr
210 215 220

Ser Phe Ala Phe Ala Val Gly Thr Thr Met Tyr Leu Val Gly Arg Ser
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Tyr Ser Thr Arg Lys Trp Tyr Leu Ser Lys Phe Glu Asp Phe Pro Lys

His Val Lys Ala Val Ile Pro Phe Val Phe
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<213> *Arabidopsis thaliana*

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35 40 45

Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp
50 55 60

Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp
65 70 75 80

Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Gly Arg Gly Gly Gly Glu
85 90 95

Gly Arg Gly Asn Ala Asp Ala Thr Phe Thr Tyr Arg Pro Ser Val Pro
100 105 110

Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe
115 120 125

Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile
130 135 140

Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp
145 150 155 160

Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp
165 170 175

Pro Leu Phe Met Cys Cys Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala
180 185 190

Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val
195 200 205

Val Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro
210 215 220

Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr

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His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala			
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Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe			
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Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu			
435	440	445	
Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu			
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Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln			
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485

490

495

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Asn	Gly	Ser	Leu	Ala	Ser	Ser	Arg	Arg	Ser	Ser	Phe	Ala	Gln	Asn	Gly	20	25	30	
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Val	His	Thr	Ala	Gln	Asp	Ser	Leu	Phe	Ser	Thr	Ser	Ser	Gly	Trp	Thr	50	55	60	
Asn	Phe	Arg	Gly	Phe	Phe	Asn	Leu	Ser	Ile	Leu	Leu	Leu	Val	Leu	Ser	65	70	75	80
Asn	Gly	Arg	Val	Ala	Leu	Glu	Asn	Val	Ile	Lys	Tyr	Gly	Ile	Leu	Ile	85	90	95	
Thr	Pro	Leu	Gln	Trp	Ile	Ser	Thr	Phe	Val	Glu	His	His	Tyr	Ser	Ile	100	105	110	
Trp	Ser	Trp	Pro	Asn	Leu	Ala	Leu	Ile	Leu	Cys	Ser	Asn	Ile	Gln	Ile	115	120	125	
Leu	Ser	Val	Phe	Gly	Met	Glu	Lys	Ile	Leu	Glu	Arg	Gly	Trp	Leu	Gly	130	135	140	
Asn	Gly	Phe	Ala	Ala	Val	Phe	Tyr	Thr	Ser	Leu	Val	Ile	Ala	His	Leu	145	150	155	160
Thr	Ile	Pro	Val	Val	Val	Thr	Leu	Thr	His	Lys	Trp	Lys	Asn	Pro	Leu	165	170	175	
Trp	Ser	Val	Val	Met	Met	Gly	Val	Tyr	Val	Ile	Glu	Ala	Leu	Lys	Phe	180	185	190	
Ile	Ser	Tyr	Gly	His	Val	Asn	Tyr	Trp	Ala	Arg	Asp	Ala	Arg	Arg	Lys	195	200	205	
Ile	Thr	Glu	Leu	Lys	Thr	Gln	Val	Thr	Asp	Leu	Ala	Lys	Lys	Thr	Cys	210	215	220	
Asp	Pro	Lys	Gln	Phe	Trp	Asp	Leu	Lys	Asp	Glu	Leu	Ser	Met	His	Gln	225	230	235	240
Met	Ala	Ala	Gln	Tyr	Pro	Ala	Asn	Leu	Thr	Leu	Ser	Asn	Ile	Tyr	Tyr	245	250	255	

Phe Met Ala Ala Pro Thr Leu Cys Tyr Glu Phe Lys Phe Pro Arg Leu		
260	265	270
Leu Arg Ile Arg Lys His Phe Leu Ile Lys Arg Thr Val Glu Leu Ile		
275	280	285
Phe Leu Ser Phe Leu Ile Ala Ala Leu Val Gln Gln Trp Val Val Pro		
290	295	300
Thr Val Arg Asn Ser Met Lys Pro Leu Ser Glu Met Glu Tyr Ser Arg		
305	310	315 320
Cys Leu Glu Arg Leu Leu Lys Leu Ala Ile Pro Asn His Leu Ile Trp		
325	330	335
Leu Leu Phe Phe Tyr Thr Phe Phe His Ser Phe Leu Asn Leu Ile Ala		
340	345	350
Glu Leu Leu Arg Phe Ala Asp Arg Glu Phe Tyr Arg Asp Phe Trp Asn		
355	360	365
Ala Glu Thr Ile Gly Tyr Phe Trp Lys Ser Trp Asn Ile Pro Val His		
370	375	380
Arg Phe Ala Val Arg His Ile Tyr Ser Pro Met Met Arg Asn Asn Phe		
385	390	395 400
Ser Lys Met Ser Ala Phe Phe Val Val Phe Phe Val Ser Ala Phe Phe		
405	410	415
His Glu Tyr Leu Val Ser Val Pro Leu Lys Ile Phe Arg Leu Trp Ser		
420	425	430
Tyr Tyr Gly Met Met Gly Gln Ile Pro Leu Ser Ile Ile Thr Asp Lys		
435	440	445
Val Val Arg Gly Gly Arg Thr Gly Asn Ile Ile Val Trp Leu Ser Leu		
450	455	460
Ile Val Gly Gln Pro Leu Ala Ile Leu Met Tyr Gly His Asp Trp Tyr		
465	470	475 480
Ile Leu Asn Phe Gly Val Ser Ala Val Gln Asn Gln Thr Val Gly Ile		
485	490	495

<210> 15
<211> 257
<212> DNA
<213> Glycine max

<400> 15
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cctcttgggg gatctaagaa aaagctacta aatgtgtggg ttgttttcac atttgttgca 180
atctggcatg atttagagtg gaagcttctt tcatgggcat ggttgacgtg tttattcttc 240
atccctgagt tggtttt 257

<210> 16
<211> 234
<212> DNA
<213> Glycine max

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atatttacag gagttatggg atttataata gaacaatata ttaatcccat tgtacaaaat 180
tcacagcatc ctctcaaggg aaaccttctt tacgccatcg agagagttct gaag 234

<210> 17
<211> 275
<212> DNA
<213> Glycine max

<220>
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<222> (192)
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<222> (238) .. (239)
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<222> (244) .. (245)
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<222> (251)
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<222> (262) .. (263)
<223> n=a, t, c or g

<400> 17

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gatgatccgc cacctatatt ttccatgttt aaggcacggg ataccaaagg ccgttgctct 120
tttaattgcc ttcttggttc tgctttattc catgagctgt gcacgcgtgt tccttgccca 180
catattcaag tngtgggttt cngnggaatt nagtttcagg tnccttgggt ttenaccnna 240
attnntnggc naaaaaattc cnngaacccc ggggg 275
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<210> 18

<211> 267

<212> DNA

<213> Glycine max

<400> 18

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ctgcttttgt atctgggtgc acgttgatgc tattaacttg cattgtgtgg ttaaaattgg 60
tgtcatatgc acatacaaac tatgatatga gagcacttac tgtttcgaat gaaaagggag 120
aaacattacc caatactttg atatggagta tccgtacact gtgaccttca ggagtttggc 180
atacttcatg gttgctccta cattatgcta tcagacaagc taccctcgca caccttcagt 240
tcgaaagggg tgggtgtttc gtcaact 267
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<210> 19

<211> 1895

<212> DNA

<213> Human

<220>

<221> unsure

<222> (209)

<223> n=a, t, c or g

<400> 19

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tgggtgctga gtctcagagc ttggcatgga gaccagacag ggctgggtct gcaagcctga 120
ggctgccgcc ctgagctcgg gctggggactg gccagaggt gttgggagga tctgggggtga 180
gtacctgtg gccaggacta aaggggctnc accctcctgt ccatccctcg cagatcttga 240
gcaatgcccc gttatttctg gagaacctca tcaagtatgg catcctgggtg gaccccatcc 300
aggtgggtttc tctgttctg aaggatccct atagctggcc cgccccatgc ctgggtattg 360
cggccaatgt ctttgcctg gctgcattcc aggttgagaa gcgcctggcg gtgggtgccc 420
tgacggagca ggccgggactg ctgctgcacg tggccaacct ggccaccatt ctgtgtttcc 480
cagcggctgt ggtcttactg gttgagtcta tcaactcagt gggctccctg ctggcgctga 540
tggcgcacac catcctcttc ctcaagctct tctcctaccg cgacgtcaac tcatggtgcc 600
gcagggccag ggccaaggct gcctctgcag ggaagaaggc cagcagtgtc gctgccccgc 660
acaccgtgag ctaccgggac aatctgacct accgcgatct ctactacttc ctcttcgccc 720
ccacctgtg ctacgagctc aactttcccc gctctccccg catccggaag cgctttctgc 780
tgcgacggat ccttgagatg ctgttcttca cccagctcca ggtggggctg atccagcagt 840
ggatgggtccc caccatccag aactccatga agcccttcaa ggacatggac tactcacgca 900
tcacgagcgc ctcctgaag ctggcggtcc ccaatcacct catctggctc atcttcttct 960
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actggctctt ccactcctgc ctgaatgccg tggctgagct catgcagttt ggagaccggg 1020
 agttctaccg ggactggtgg aactccgagt ctgtcaccta cttctggcag aactggaaca 1080
 tccctgtgca caagtgggtgc atcagacact tctacaagcc catgcttcga cggggcagca 1140
 gcaagtggat ggccaggaca ggggtgttcc tggcctcggc cttcttccac gagtacctgg 1200
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 tcaactatga ggccccagcg gcagaggcct gagctgcacc tgagggcctg gcttctcact 1440
 gccacctcac acccgctgcc agagcccacc tctcctccta ggcctcgagt gctggggatg 1500
 ggcttggtg cacagcatcc tcctctggtc ccagggaggc ctctctgccc ctatggggct 1560
 ctgtcctgca cccctcaggg atggcgacag caggccagac acagtctgat gccagctggg 1620
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 ccagagctgt gtggacagct gtcccaggac ctgccgggga gcagcagctc cactgcagca 1800
 gggcgggcat ggccggtagg gggagtgcaa ggccaggcag acgcccccat tccccacact 1860
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<210> 20
 <211> 519
 <212> DNA
 <213> Montierella alphina

<220>
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 <223> n=a, t, c or g

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 <221> unsure
 <222> (22)
 <223> n=a, t, c or g

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 <222> (46)
 <223> n=a, t, c or g

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<222> (64)
<223> n=a, t, c or g

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<222> (68)
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<222> (82)..(84)
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<222> (102)..(103)
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<222> (113)
<223> n=a, t, c or g

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<222> (148)

<223> n=a, t, c or g

<220>

<221> unsure

<222> (430)

<223> n=a, t, c or g

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ttanactnaa ttngaaaatn cnmcccaac ttnaggnact tnnagncccc ccnacttgac 120
aacggagcac tatatttacc ccgtggtngt tcaaccacgc catctcaccg ttgcgagcat 180
tggtgctgct cttgataccc ttcattgctta actatctcat gatcttttac atcattttcg 240
agtgcacatg caacgccttt gcggaactaa gttgctttgc ggatcgcaac ttttacgagg 300
attggtggaa ctgcgtcagc tttgatgagt gggcacgcaa atggaacaag cctgtgcaac 360
acttcttgct ccgccacgtg tacgactcga gcatecgagt ccttccactt gtccgaaatc 420
caatgccgcn aattgcaaac gttccttccc ggtegtcaat gcgttcaacg aacctggggtg 480
aagaatgggt ggtgacaacg ttaaagtgcg cccggtatc 519
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<210> 21

<211> 518

<212> DNA

<213> mouse

<400> 21

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attcggcacg atggggcacga ggactccatc atgttctca agctttattc ctaccgggat 120
gtcaacctgt ggtgccgcca gcgaaggggc aaggccaaag ctgtctctac agggaagaag 180
gtcagtgggg ctgctgagag caagctgtga gctatccaga caacctgacc taccgagatc 240
tcgattactt catctttgct cctactttgt gttatgaact caactttcct cggccccccc 300
gaatacgaga gcgctttctg ctacgacgag ttcttgagat gctctttttt acccagcttc 360
aagtggggct gatccaacag tggatgggtc ctactatcca gaactccatg gaagcccttt 420
caagagcttc tgcagttttg gagaccgca gttctacaga gattggtgga atgctgagtc 480
tgtcaccgac ttttggcaga actggaatat ccccgtagg 518
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<210> 22

<211> 299

<212> DNA

<213> mouse

<400> 22

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ccatgatggc tcaggtccca ctggcctgga ttgtgggccc attcttccaa gggaaactatg 60
gcaatgcagc tgtgtgggtg aactcatca ttgggcaacc ggtggctgtc tcatgtatgt 120
ccacgactac tacgtgtcga actacgatgc cccagtgggt catgagctac tgccaaaggc 180
agccctccct aacctgggcc tggagtcttg gaggggttcc tggctgcctg cacactcctc 240
ctagtctggg aggcctctct gccctatgc gctactcctg ctcttgggga tggcatttg 299
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<210> 23
 <211> 1766
 <212> DNA
 <213> Rat

<400> 23
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 tagacgaaga ggaggtgcga gacgccgctg tgggccccga cttgggcgcc gggggtgacg 180
 ctccggctcc ggctccgggt ccggctccag cccacacccg ggacaaaagac cggcagacca 240
 gcgtgggcga cggccactgg gagctgaggt gccatcgtct gcaagactct ttgttcagct 300
 cagacagcgg tttcagcaat taccgtggta tctgaattg gtgcgtgggtg atgctgatcc 360
 tgagtaatgc aaggttatct ttagagaatc ttatcaagta tggcatcctg gtggatccca 420
 tccaggtggg gtctctgttt ctgaaggacc cctacagctg gcctgccccca tgcttgatca 480
 ttgcatccaa tatctttatt gtggctacat ttcagattga gaagcgctg tcagtgggtg 540
 ccctgacaga gcagatgggg ctgctgctac atgtgggtta cctggccaca attatctgct 600
 tcccagcagc tgtggcctta ctggttgagt ctatcactcc agtgggttcc ctgtttgctc 660
 tggcatcata ctccatcctc ttctcaagc ttttctccta ccgggatgtc aatctgtggg 720
 gccgccagcg aagggtcaag gccaaagctg tgtctgcagg gaagaagggtc agtggggctg 780
 ctgcccagaa cactgtaagc tatccggaca acctgacctc ccgagatctc tattacttca 840
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 gctttctgct acggcggggt cttgagatgc tctttttcac ccagcttcaa gtggggctga 960
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 tcttcttcta ttggcttttc cactcatgtc tcaatgctgt ggcagagctc ctgcagtttg 1140
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 agctatctaa aaaaaaaaaa aaaaaa 1766

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 <211> 500
 <212> PRT
 <213> rat

<400> 24
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Ser Arg Val Ser Ile Gln Gly Gly Ser Gly Pro Met Val Asp Glu Glu
 20 25 30

Glu Val Arg Asp Ala Ala Val Gly Pro Asp Leu Gly Ala Gly Gly Asp
 35 40 45

Ala Pro Ala Pro Ala Pro Val Pro Ala Pro Ala His Thr Arg Asp Lys
 50 55 60

Asp Arg Gln Thr Ser Val Gly Asp Gly His Trp Glu Leu Arg Cys His
 65 70 75 80

Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
 85 90 95

Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala
 100 105 110

Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro
 115 120 125

Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala
 130 135 140

Pro Cys Leu Ile Ile Ala Ser Asn Ile Phe Ile Val Ala Thr Phe Gln
 145 150 155 160

Ile Glu Lys Arg Leu Ser Val Gly Ala Leu Thr Glu Gln Met Gly Leu
 165 170 175

Leu Leu His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala
 180 185 190

Val Ala Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Leu Phe Ala
 195 200 205

Leu Ala Ser Tyr Ser Ile Ile Phe Leu Lys Leu Phe Ser Tyr Arg Asp
 210 215 220

Val Asn Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser
 225 230 235 240

Ala Gly Lys Lys Val Ser Gly Ala Ala Ala Gln Asn Thr Val Ser Tyr
 245 250 255

Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro
 260 265 270

Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys
275 280 285

Arg Phe Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu
290 295 300

Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile Gln Asn Ser
305 310 315 320

Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu
325 330 335

Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr
340 345 350

Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe
355 360 365

Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr
370 375 380

Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg
385 390 395 400

His Phe Tyr Lys Pro Met Leu Arg Leu Gly Ser Asn Lys Trp Met Ala
405 410 415

Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val
420 425 430

Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met
435 440 445

Ala Gln Val Pro Leu Ala Trp Ile Val Asn Arg Phe Phe Gln Gly Asn
450 455 460

Tyr Gly Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val
465 470 475 480

Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala
485 490 495

Pro Val Gly Ala
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<210> 25

<211> 325

<212> DNA
<213> Zea mays

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<222> (304)

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<222> (317)

<223> n=a, t, c or g

<220>

<221> unsure

<222> (321)

<223> n=a, t, c or g

<400> 25

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aagatatctc catgctacgt tcaagcatgt aatgggtggc aacatgatan tttggntctn 180
cagtatagtc ggacagccga tgtnnnnnna tctatactac catgacgtca tgaacaggca 240
ggcccaggca agtagatagt ncggcagaga catgtacttc aacatcganc atcagnagca 300
nacngagcga gcggcangaa ncagc 325
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<210> 26

<211> 262

<212> DNA

<213> Zea mays

<400> 26

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gccactgcta atgtgttgcc ttagtctacc catatttccc cttggtgcat ttgcagtcga 120
aaagttggca ttcaacaatc tcattagtga tctgtact acctgttttc acatcctttt 180
tacaacattt gaaattgtat atccagtgtc cgtgattctt aagtgtgatt ctgcagtttt 240
acaggctttg tgttgatgtt ta 262
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<210> 27
 <211> 253
 <212> DNA
 <213> Zea mays

<400> 27
 agaaaatgga acatgcctgt gcataaatgg attgttcgtc atatataatt tccttgcatg 60
 cgaaatggta tatcaaagga agttgctgtt tttatatcgt tcttgtttct gctgtacttc 120
 atgagttatg tgttgctgtt ccctgccaca tactcaagtt ctgggctttt ttttaggaatc 180
 atgcttcaga ttccctcat catattgaca tcataacctca aaaataaatt cagtgcacaca 240
 atggttgga ata 253

<210> 28
 <211> 254
 <212> DNA
 <213> Zea mays

<400> 28
 tgaagtatgg cttattaata agatctggct tttggtttaa tgctacatca ttgcgagact 60
 ggccactgct aatgtgttgc cttagtctac ccatatttcc ccttggtgca tttgcagtcg 120
 aaaagttggc attcaacaat ctcatagtg atcctgctac tacctgtttt cacatccttt 180
 ttacaacatt tgaaattgta tatccagtgc tcgtgattct taagtgtgat tctgcagttt 240
 tatcaggctt tgtg 254

<210> 29
 <211> 1645
 <212> DNA
 <213> Maize

<400> 29
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 cgccgcggcg gaggcgctgg ccaagggcgg cgtggagacg gtgctgatcg agcgggaagat 120
 ggacaactgc aagccctgcg gggcgctat cccgctgtgc atggtgtcgg agttcgacct 180
 gccgctcgac ctctgtggacc gcaaggtgag gaagatgaag atgatttcgc cgtccaacgt 240
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 ggtgctcgac gctacctec gctcacgggc acagtccgtc ggcgcgagg tcgtcaacgg 360
 cctcttcta aggtacgagg cgcccaaaga gccgaacggc tcgtacgtgg tgcactacaa 420
 ccactacgac ggcagcaacg gcaaggtcgg cggcgagaag cggctcgttcg aggtggacgc 480
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 cgagtacgcc atcgcttcc aggagcgcgt caagatcccc gacgacaaga tgggtgtacta 600
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 gttccccaag tgcgaccag tcgccgtcgg caccggcacc gtcacgcaca aggccgacat 720
 caagaagttt caggccgcca cgcgcctccg cgccaaggac aagattgagg gcggcaagat 780
 catccgcgtc gaggcgacc ccattcccga gcacccagg cctaagaggg tgtccgggcg 840
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cttcgcgggcg aagagcgggc ggatgtgcg cgaggccatc gtggcgggct ccgccaacgg 960
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ctggcccaact tacaagggtgc tggacatcct gcagaagggtg ttctaccgct ccaacgcggc 1080
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atcgactgga ttctgacgcc ggcaagcatc gacgtcaatg aatgtctaata acttagtaca 1560
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<210> 30
<211> 541
<212> PRT
<213> Maize

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<220>
<221> UNSURE
<222> (414)
<223> Xaa=any amino acid

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<220>
<221> UNSURE
<222> (445)
<223> Xaa=any amino acid

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<220>
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<223> Xaa=any amino acid

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<220>
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<220>
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<220>
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<223> Xaa=any amino acid

<220>

<221> UNSURE

<222> (520)

<223> Xaa=any amino acid

<400> 30

Leu Arg Val Ala Val Val Gly Gly Gly Pro Ala Gly Gly Ala Ala Ala
1 5 10 15

Glu Ala Leu Ala Lys Gly Gly Val Glu Thr Val Leu Ile Glu Arg Lys
20 25 30

Met Asp Asn Cys Lys Pro Cys Gly Gly Ala Ile Pro Leu Cys Met Val
35 40 45

Ser Glu Phe Asp Leu Pro Leu Asp Leu Val Asp Arg Lys Val Arg Lys
50 55 60

Met Lys Met Ile Ser Pro Ser Asn Val Ala Val Asp Ile Gly Arg Thr
65 70 75 80

Leu Ala Pro His Glu Tyr Ile Gly Met Val Arg Arg Glu Val Leu Asp
85 90 95

Ala Tyr Leu Arg Ser Arg Ala Gln Ser Val Gly Ala Glu Val Val Asn
100 105 110

Gly Leu Phe Leu Arg Tyr Glu Ala Pro Lys Glu Pro Asn Gly Ser Tyr
115 120 125

Val Val His Tyr Asn His Tyr Asp Gly Ser Asn Gly Lys Val Gly Gly
130 135 140

Glu Lys Arg Ser Phe Glu Val Asp Ala Ile Val Gly Ala Asp Gly Ala
145 150 155 160

Asn Ser Arg Val Ala Asn Asp Met Gly Ala Gly Asp Tyr Glu Tyr Ala
165 170 175

Ile Ala Phe Gln Glu Arg Val Lys Ile Pro Asp Asp Lys Met Val Tyr
180 185 190

Tyr Glu Glu Arg Ala Glu Met Tyr Val Gly Asp Asp Val Ser Pro Asp
195 200 205

Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp His Val Ala Val Gly Thr

210	215	220
Gly Thr Val Thr His Lys Ala Asp Ile Lys Lys Phe Gln Ala Ala Thr		
225	230	235 240
Arg Leu Arg Ala Lys Asp Lys Ile Glu Gly Gly Lys Ile Ile Arg Val		
	245	250 255
Glu Ala His Pro Ile Pro Glu His Pro Arg Pro Lys Arg Val Ser Gly		
	260	265 270
Arg Val Thr Leu Val Gly Asp Ala Ala Gly Tyr Val Thr Lys Cys Ser		
	275	280 285
Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser Gly Arg Met Cys Ala Glu		
	290	295 300
Ala Ile Val Ala Gly Ser Ala Asn Gly Thr Arg Met Val Glu Glu Ser		
	305	310 315 320
Asp Leu Arg Lys Tyr Leu Ala Glu Phe Asp Arg Leu Tyr Trp Pro Thr		
	325	330 335
Tyr Lys Val Leu Asp Ile Leu Gln Lys Val Phe Tyr Arg Ser Asn Ala		
	340	345 350
Ala Arg Glu Ala Phe Val Glu Met Cys Ala Asp Asp Tyr Val Gln Lys		
	355	360 365
Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg Val Val Pro Gly Asn Pro		
	370	375 380
Leu Asp Asp Ile Lys Leu Ala Val Asn Thr Ile Gly Ser Leu Val Arg		
	385	390 395 400
Ala Thr Ala Leu Arg Arg Glu Met Glu Lys Val Thr Leu Xaa Ala Ala		
	405	410 415
Ala Arg Asp Val Ile Ala Val Glu Met Val Ser Gln Leu Ile Gly Arg		
	420	425 430
Cys Ile Ser Arg Asp Leu Arg Leu Ile Gly Leu Ile Xaa Ala Asn Met		
	435	440 445
Arg Gly Gln Trp Ala Arg Arg Gly Arg Glu Thr Ser Cys Ala Ser Ala		
	450	455 460
Ala Ser Arg Ser Lys Val Leu Pro Val Cys Ile Asp Gly Ser Cys Asn		

465	470	475	480
Ile Xaa His Leu Val Met Leu Arg Ile Arg Ser Ser Ser Ser Thr Gly			
485	490	495	
Phe Xaa Arg Arg Gln Ala Ser Thr Ser Met Asn Val Xaa Tyr Leu Val			
500	505	510	
His Gln Asp Met Xaa Xaa Asn Xaa Asn Ser Pro Val Leu Val Gln Lys			
515	520	525	
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Gly Arg			
530	535	540	

<210> 31
 <211> 80
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: transit peptide

<400> 31
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 Ala Gly Ala Gly Met Val Ala Pro Phe Thr Gly Leu Lys Ser Met Ala
 20 25 30
 Gly Phe Pro Phe Thr Gly Leu Lys Ser Met Ala Gly Phe Pro Thr Arg
 35 40 45
 Lys Thr Asn Asn Asp Ile Thr Ser Ile Ala Ser Asn Gly Gly Arg Val
 50 55 60
 Gln Cys Met Gln Val Trp Pro Pro Ile Gly Lys Lys Lys Phe Glu Thr
 65 70 75 80